





SOURCE	thale cress.
ORGANISM	<i>Arabidopsis thaliana</i>
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. (bases 1 to 206)
AUTHORS	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE	A large scale analysis of cDNA in <i>Arabidopsis thaliana</i> : Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL	DNA Res. 7, 175-180 (2000)
MEDLINE	20363093
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
FEATURES	Location/Qualifiers
SOURCE	1. . 206 'organism'='Arabidopsis thaliana' 'strain'='Columbia' 'db_xref'='taxon:3702' 'clone'='SO13405F' 'clone_id'='Arabidopsis thaliana green siliques' 'tissue_type'='green siliques' 'note'='Vector: pBluescriptII SK-'; Site_1: EcoRI; Site_2: XbaI' ORIGIN
BASE COUNT	69 a 43 c 28 g 66 t.
RESULT	5
LOCUS	BE498304/c
DEFINITION	WHE0963_B10_C19zs Wheat pre- <sup>-</sup> synthesis spike cDNA library
ACCESSION	WHE0963_B10_C19zs
VERSION	0
KEYWORDS	EST.
SOURCE	bread wheat.
ORGANISM	<i>Triticum aestivum</i>
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; <i>Triticum</i> ; <i>Triticum</i> ; <i>Triticum</i> .	
REFERENCE	1 (bases 1 to 505)
AUTHORS	Anderson,O.D., Chao,S.S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
TITLE	The structure and function of the expressed portion of the wheat genomes - Pre- <sup>-</sup> synthesis spike cDNA library
JOURNAL	Unpublished (2000)
COMMENT	Contact: Olin Anderson



Db	191	CCGGCGCTTGGACACGCCCTCTTCCAGAAGAAACCCCTGGTTGGTCCGGATCA 132
Qy	731	acggatcaagaacgtctccaaactctgtttactataaagggtctct 779
Db	142	ACGCTGGTTCAGAGATACTGCTGGTGGAGCCAACTCCATGCCATGAAACAGGCCCTC 83
Qy	131	AGGGTCCAGCACCTCCCCACACCTGGCCAAACCCAGGGTCTCTC 83
Db	82	CCATCATACATCACAGTTAGAGCACTGAGCTAACAAATGGGTTCTAGAACATCTCCAC 23
RESULT	7	AV937451
LOCUS		AV937451 542 bp mRNA linear EST 18-JAN-2002
DEFINITION		AV937451 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah1n08 5', mRNA sequence.
ACCESSION		AV937451
VERSION		AV937451.1
KEYWORDS		Hordeum vulgare subsp. spontaneum EST.
ORGANISM		Hordeum vulgare subsp. spontaneum. Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta; Tridiliplanteae; Poales; Poaceae; Pooidae.
REFERENCE		1 (bases 1 to 542)
AUTHORS		Sato, K., Saisho, D. and Takeda, K.
TITLE		EST sequencing project in NIG and Okayama Univ
JOURNAL		Unpublished (2002)
COMMENT		Contact: Tadasu Shin-1 Center for Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.
FEATURES	source	1. .542 location/Qualifiers
BASE COUNT	120	a 150 c 146 g 124 t 2 others
ORIGIN		
Query Match		21.6%; Score 184; DB 9; Length 542; Best Local Similarity 62.6%; Pred. No. 1.1e-21; Matches 303; Conservative 0; Mismatches 180; Indels 1; Gaps 1;
Qy	274	ctcttcctcccgagccacctccctcgacaaatgttggaaactgcggccaggaa 333
Db	502	crcctccggccgtggccgtggacggcgtggcAGGTCTGAAGTACACGGCGCGACGGGCTTG 443
Qy	334	cgagatgttagatctcgacaaactcgcgaggttgttggatctggccggccacctgtgtca 393
Db	442	CCAGGTGAAGGGCGCCGAAGCTGGTGAAGCTCTGGCCCTGGCG 383
Qy	394	tacactttgtcgccaaactgtcgacaaataataacacgacacatgttgcgtgtca 453
Db	382	AACACCGGCCGCCAGCTCGTGTACAGACACATAACATGGGGATGCCATA 323
Qy	454	gtggacttggatttcgttgcacacaaatcttcattggccaaagggttccagtgttgcgtgtca 513
Db	262	GGGACATCGTCACCAACCAAGTCAGGTTCTCCCTCAGGGTGGTGGGATTAGSC 203
Qy	574	aatctgtgtggccacccatcacaaccaaaatgttgcgtgggttcaccaatctca 633
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LOCUS		BG647258 EST08867 HOGA Medicago truncatula cDNA clone PHOGA-1619 5', end, mRNA sequence.
DEFINITION		BG647258
ACCESSION		BG647258.1
VERSION		GT:13782360
KEYWORDS		EST.
ORGANISM		Medicago truncatula. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosids; eurosids I; Fabales; Fabaceae; Papilioideae; Trifolieae; Medicago.
REFERENCE		1 (bases 1 to 781)
AUTHORS		Hahn, M.G., Ojanen-Rehbs, T., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
TITLE		ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20
JOURNAL		Unpublished (2001)
COMMENT		Contact: Michael G. Hahn University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: hahn@ccrc.uga.edu
FEATURES	source	G390854e TIGR sequence name: MTBMW53TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gaa CTA gtg gat cc). Location: SKmod (CTA gaa CTA gtg gat cc).
BASE COUNT	243	a 147 c 150 g 241 t
ORIGIN		
Query Match		21.1%; Score 181; DB 10; Length 781; Best Local Similarity 59.4%; Pred. No. 3.7e-21; Matches 326; Conservative 0; Mismatches 220; Indels 3; Gaps 1;
Qy	251	taaagaagaacccatcaaaatgttccctccggccactctccctgttgcataatgt 310





Query Match 16.7%; Score 143; DB 10; Length 574;  
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 Matches 236; Conservative 0; Mismatches 155; Indels 0; Gaps 0;  
 BASE COUNT 150 a 141 c 131 g 152 t  
 ORIGIN

Query Match 16.6%; Score 142.2; DB 12; Length 773;  
 Best Local Similarity 76.7%; Pred. No. 1.2e-14;  
 Matches 174; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

LOCUS BF259482 574 bp mRNA linear EST 22-OCT-2001  
 DEFINITION HSMEF019p18f Hordeum vulgare seedling root EST library HVCDA0007  
 (Etiolated and unstressed) Hordeum vulgare cDNA clone  
 ACCESSION BF259482  
 VERSION BF259482.2 GI:13119945  
 KEYWORDS EST.  
 ORGANISM Hordeum vulgare.  
 SOURCE  
 Bokarvota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
 ; Triticeae; Hordeum.  
 REFERENCE 1. (bases 1 to 574)  
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R., and Main, D.  
 Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library  
 Unpublished (2001)  
 On Nov 16, 2000 this sequence version replaced gi:11188511.  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7208  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hq bases = 426  
 Seq primer: AATPACCCCTACTAAAGGG  
 High quality sequence stop: 572.  
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 1. .574  
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 /clone="HSMEF019p18f"  
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 /tissue\_type="Seedling root"  
 /lab\_host="TICL21"  
 /note="vector: lambdaZAP; Site:1: EcoRI; Site: 2: XbaI;  
 Seeds were surface sterilized then germinated under axenic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered  
 crystallization dishes. Five-day old seedling roots were  
 then harvested, total RNA was prepared, poly(A) RNA was  
 purified, one primary unamplified cDNA library was made,  
 and 1 million pfu were *in vivo* excised to give pBluescript  
 SK(-) DNA phagemids. These steps were performed in the TJ  
 Close laboratory at the University of California,  
 Riverside (Choi, Close, Fenton). Phagemids were plated and  
 picked at the Clemson University Genomics Institute (CUGI)  
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA  
 preparations, DNA sequencing and sequence analysis were  
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates  
 , Rambo, Main). The sequence has been trimmed to remove  
 vector sequence and contains a minimum of 100 bases of  
 phred value 20 or above. For more details on library  
 preparation and sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
 this clone see <http://www.genome.clemson.edu/orders> Also  
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>).

RESULT 13  
 BH42868/c  
 LOCUS BH42868 773 bp DNA linear GSS 14-DEC-2001  
 DEFINITION BOGJN29F BOGJ Brassica oleracea genomic clone BOGJN29, DNA  
 sequence.  
 SOURCE  
 GSS.  
 ORGANISM Brassica oleracea.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1. (bases 1 to 773)  
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.  
 AUTHORS  
 TITLE Whole genome shotgun sequencing of *Brassica oleracea*  
 JOURNAL Unpublished (2001)  
 COMMENT Other:GSS: BOGJN29TR  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: catown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.  
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 /clone="BOGN29"  
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 genomic DNA inserted into phosI using BstXI linkers"



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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NP011508RT"
/clone_id="Developing root"
/tissue_type="root"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Total RNA was extracted from
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medium. Samples were taken at four time points
(approximately two days, one, two and six weeks post
germination) representing early seedling growth to
nitrogen limitation."

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Search completed: September 14, 2002, 18:25:04  
Job time: 23469 sec









US 08-482-130C-60

Query Match, 5.5%; Score 46.8; DB 2; Length 234; Best Local Similarity 73.2%; Pred. No. 0.0011; Matches 60; Conservatve 0; Mismatches 22; Indels 0; Gaps 0;

Qy 775 tcctttatattatagacatctttgatcttgacaaacactcggtgtgatccgtggacc 834  
 Db 129 TATCTGTAGATGAGACGCCCTAATCCAAACCAACGCTGAGTCAGCC 70

Qy 835 cggggatccactatgttctaga 856  
 Db 69 CGGGGATCCACTATGTCTAGA 48

RESULT 8

US-08-484-211C-60/c  
 Sequence 60 Application US/08484211C

PATENT NO. 5972645

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wu Hunter, Shirley

APPLICANT: Frank, Glenn R.

APPLICANT: Stieger, Gary L.

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID

TITLE OF INVENTION: MOLECULES, AND USES THEREOF

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross P.C.

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,211C

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 234 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..234

US-08-484-211C-60

US 08-639-075

Query Match, 5.5%; Score 46.8; DB 3; Length 234; Best Local Similarity 73.2%; Pred. No. 0.0011; Matches 60; Conservatve 0; Mismatches 22; Indels 0; Gaps 0;

Qy 775 tcctttatattatagacatctttgatcttgacaaacactcggtgtgatccgtggacc 834  
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Qy 835 cggggatccactatgttctaga 856  
 Db 69 CGGGGATCCACTATGTCTAGA 48

RESULT 9

US-08-905-769-60/c  
 Sequence 60 Application US/08906769

PATENT NO. 6077637

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wu Hunter, Shirley

APPLICANT: Frank, Glenn R.

APPLICANT: Stieger, Gary

APPLICANT: Gaines, Patrick J.

APPLICANT: Silver, Gary

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID

TITLE OF INVENTION: MOLECULES AND USES THEREOF

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross &amp; McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,769

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/639,075

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 234 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..234

US-08-906-769-60

us-09-845-849-3.rni

Qy 775 tcctttatattatagacatctttgatcttgacaaacactcggtgtgatccgtggacc 834  
 Db 129 TATCTGTAGATGAGACGCCCTAATCCAAACCAACGCTGAGTCAGCC 70

Qy 835 cggggatccactatgttctaga 856  
 Db 69 CGGGGATCCACTATGTCTAGA 48

RESULT 10







GenCore version 4.5									
Copyright (c) 1993 - 2000 CompuGen Ltd.									
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Run on: September 14, 2002, 17:30:28 ; Search time 303.58 Seconds									
(without alignments) 4841.158 Million cell updates/sec									
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description	Result No.	Score	Query Length	DB ID	Description
C 1	856	100.0	856	20 AA28490	RESULT 1	1	856	20 AA28490	standard; cDNA; 856 BP.
C 2	856	100.0	856	20 AA28490	ID	AAZ2490/C	XX	AAZ2490;	
C 3	692.4	80.9	775	21 AAC4682	AC	AAZ2490;	XX	AAZ2490;	
C 4	692	80.8	754	21 AAC48359	DT	17-JAN-2000 (first entry)	XX	AAZ2490;	
C 5	528	61.7	528	21 AAC60683	DE	Flowering locus T (rn) gene.	XX	AAZ2490;	
C 6	377.6	44.1	528	21 AAC22966	KW	Flowering locus T gene; FT; flowering time; modulator; early flowering; antibody; cellular binding protein; crop; ss.	XX	AAZ2490;	
C 7	374.4	43.7	528	21 AA60684	KW		XX	AAZ2490;	
C 8	180.2	21.1	522	22 AAC90363	OS	Arabidopsis thaliana.	XX	AAZ2490;	
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					PD	21-OCT-1999.	XX	AAZ2490;	
					PF	13-APR-1999; 99WO-US08151.	XX	AAZ2490;	
					PR	15-APR-1998; 98US-0060726.	XX	AAZ2490;	
					PA	(SALK ) SALK INST BIOLOGICAL STUDIES.	XX	AAZ2490;	
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Db 348 TCCGAGGGGGGGGGTGCACCTCTGGTACGACACACCCATGCCAAGGGCATTCAGT 289
Qy 507 tggtagcggatccatgcaccaccaatggaaatattctcgaggtaagggtgtctagg 566
Db 288 GGTCGCAGGTATTCAGTCACCAACCTGGAGATAATCTCGTGGTGGAGGGTGCCTGG 229
Qy 567 actggacatccggatccaccaataccaaaggataggatctgggtcttccacc 626
Db 228 ACTGGCACATCTGGATCACCATAACCCAGGGTGTAGAATTCCTGAAGTCTGCTCCRC 169
Qy 627 aatctcaactttggctgtttgaacctgaaaggcttaatccaaaggccataggcacc 686
Db 168 AACCTCCATATGGTTGTCGAGCTAGTGGAGGCCTAGATCCAAAGCCATAGTAC 109
Qy 687 ctctctttggccataagtaacctttagtgtatgtatccaaaggatcgaacgtc 746
Db 108 CTCCTATGCCATAAGCACCCTAAGAGACCAACCTCGTGAAAGATCAGAACATC 49
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Db 48 TCCACACACTGCCGACACAAAGAGGATCTACGACTTAAGACAT 1

RESULT 7
AA60684/c
ID AA60684 standard; DNA; 528 BP.
XX AAA60684;
XX 26-OCT-2000 (first entry)
XX Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.
XX Arabidopsis thaliana; Cruciferae; plant; control; flowering;
KW solar radiation; ds.
XX OS Arabidopsis thaliana.
XX JP2000139250-A.
XX PD 23-MAY-2000.
XX PR 11-NOV-1998; 98JP-0320219.
XX (TORA ) TORAY IND INC.
XX WPI; 2000-425906/37.
XX A method to accelerate plant generation and generation accelerated
PT plants -
PS Claim 5; Page 5; 6pp; Japanese.
XX
the present invention describes a method to accelerate plant generation
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
XX of the present invention.
Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;

```

```

Query Match 43.7%; Score 374.4; DB 21; Length 528;
Best Local Similarity 81.8%; Pred. No. 5.2e-78;
Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
Qy 267 ctaaagtctcttcctccacggactctccctgtacaatgttagaaactcggccac 326
Db 528 CTAGTCTCTTCCTCCACAGCCATTCTCCCTGGAGTGGAGGAGGCC 469
Qy 327 ggaaggcggagatgttagatcggcaactcgatgttgaagtctggccaccc 386
Db 468 AGGAGACCAAGATGTAGATCTCAGCAACTCAGAGGTGACTGTGGCCACAC 409
Qy 387 tggtgacatactttgtgtttgttgcgttgcggaaactataacggacatgtat 446
Db 408 CGGTGATTAACCCCTTGCTTCGAGTGGCGAACATATACCAACACATAGTAC 349
Qy 447 tccgtcaatggggatctggatttgcgtacacaaatccatcccaaaatggttccagt 506
Db 348 AATTCCACATATGGTTGTCGAGACTGAGACACCCATTCGCAAGGCATTCTGG 109
Qy 687 ctctctttggccataagtaacctttagtgtatgtatccaaaggatcgaacgtc 746
Db 108 CTCCTATGCCATAAGCACCCTAAGAGACCAACCTCGTGAAAGATCAGAACATC 49
Qy 747 tccacaactctgttctataaagggtctcttattttatagacat 794
Db 48 TCCACACACTGCCGACACAAAGAGGATCTACGACTTAAGACAT 1

RESULT 8
AAC0636/c
ID AAC0636 standard; cDNA; 522 BP.
XX AAC0636;
XX DT 20-MAR-2001 (first entry)
XX DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 5.
XX KW Strawberry; flowering regulation; floral homeotic gene; field crop;
KW harvesting; fruit production; ss.
XX OS Fragaria vesca.
XX WO200071722-A1.
XX PD 30-NOV-2000.
XX PF 24-MAY-2000; 20000W0-US14297.
XX PR 25-MAY-1999; 99US-0318789.
XX PR 24-MAY-2000; 2000US-0318789.
XX (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX Oeller P, Gutterson N;
XX WPI; 2001-025165/03.
DR P-PSDB; AAB50266.
XX Novel nucleic acid involved in controlling plant flowering processes is

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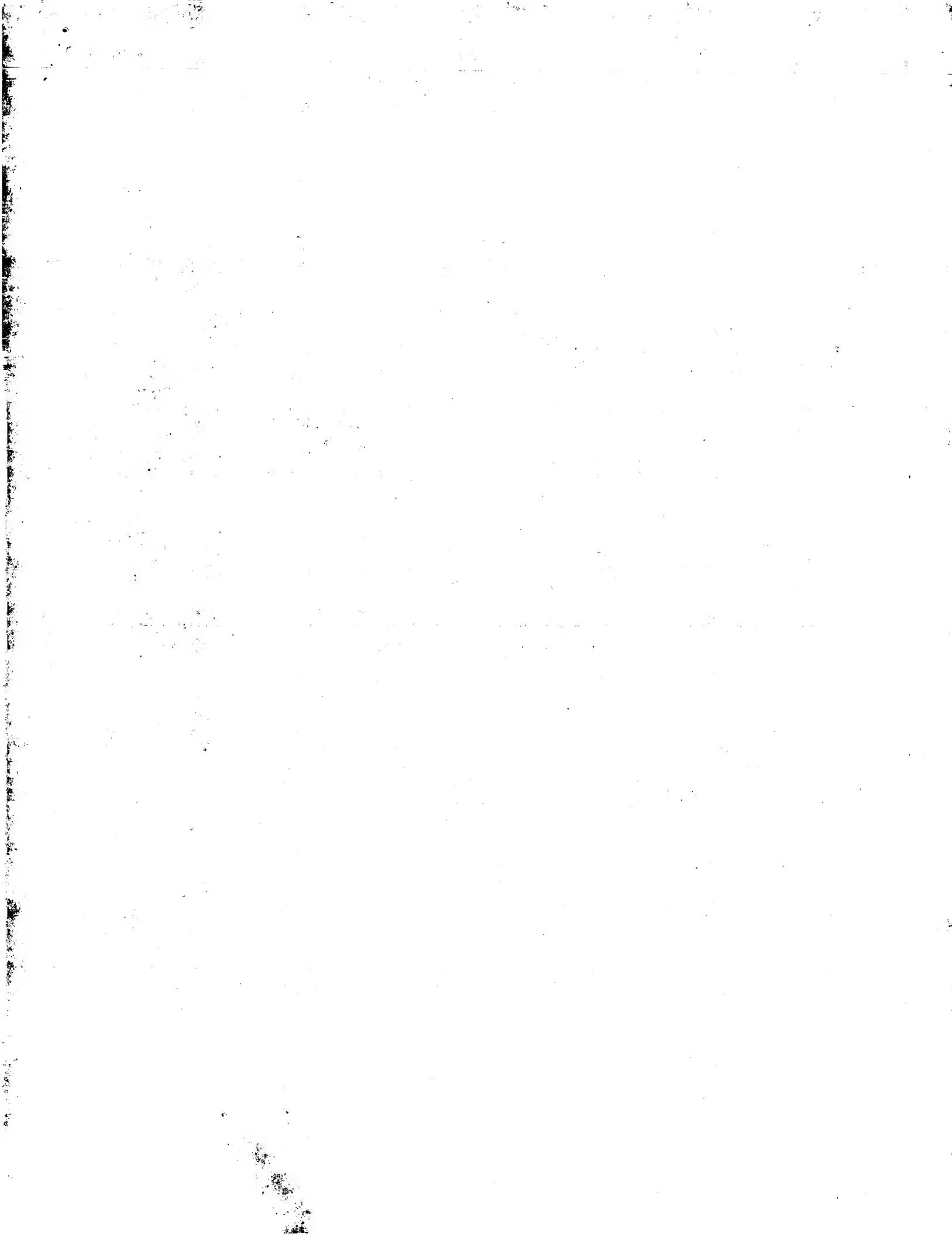




Mon Sep 16 16:43:02 2002

us-09-845-849-3.rng

Search completed: September 14, 2002, 21:21:27  
Job time: 13859 sec



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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 12:41:15 ; Search time 1868.71 Seconds (without alignments)

9585.819 Million cell updates/sec

Title: US-09-845-849-3

Perfect score: 856

Sequence: 1 ctcgagttttttttttt.....ggggatccactagttctaga 856

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_cv:\*

6: gb\_bp:\*

7: gb\_Ph:\*

8: gb\_Pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_inv:\*

ALIGMENTS

RESULT 1

AR18907 AR148907 1

AR18907 AR148907 Sequence 3 from Patent US 622530. DNA linear PAT 08-AUG-2001

DEFINITION Sequence 3 from Patent US 622530. DNA linear PAT 08-AUG-2001

LOCUS AR148907

ACCESSION AR148907

VERSION AR148907.1 01:15112997

KEYWORDS

SOURCE Unknown

ORGANISM Unclassified

REFERENCE 1 (bases 1 to 856)

AUTHORS Weigel,D. and Kardailsky,I.

TITLE Flowering Locus T (FT) and genetically modified plants having modulated flower development

FEATURES Patent: US 622550-A 3 01-MAY-2001; Location/Qualifiers

source 1. .856 /organism="unknown"

BASE COUNT 249 a 194 c 150 g 263 t

ORIGIN

Query Match 100.0%; Score 856; DB 6; Length 856;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result % Query Match Length DB ID Description

Score

No. Match

SUMMARIES











**OKAIADEKTISALLDRYETMLQKLEKEIDDDVNKIGNWRLDRSVDYDGKVKSPDEVAL**  
**KAFLWYKLGKKGQELIONLUSKDKVFFVFRMONTGGRLSEVERD.**  
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**(gene="F5114.7"**  
**complement|join|42975. . 43043|43213. . 43339, 43501. . 43593,**  
**43638. . 43711, 43856. . 44002, 44168. . 44480, 44564. . 44922))**  
**(gene="F5114.7"**  
**note="Similar to *Saccharomyces* hypothetical protein**  
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**evidence=not\_experimental**  
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**43638. . 43711, 43856. . 44002, 44168. . 44480, 44564. . 44922))**  
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**note="Similar to *zea mays* permease 1 (gb|U43034)."**  
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**TLFOSPFTRLVIVAYVAVIPTISLISYRFTYDPTPFLVFRMVTGQTL**  
**GGFOVLICILGWRNVTYRFLSPSLIATLAFNGLGLWHGFLDLYNNMOTSIQFLAR**  
**CEVGLDHLFLFVOTDPLRFLPKMKGVMILDSRDFYGMCLPFLWFLWPAQLTS**  
**FESTGLTYASRNGSAIPPPSVSRSGTCLWGLGVGLNGMIGGITGTTENGLIA**  
**MTKIGSRVQVTOISAAFMFSFSGKCAFASFLPLPIMASLICIVLGCFVCKFSHII**  
**CSAFCISNCFIETQVQVAAASVYASVGLSLQFCNUNSNFKEFLGFFMAISIP**  
**QFREYIYNGWSDHHSWNSVSYSL"**  
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**(gene="F5114.9"**  
**complement|join|50678. . 51059|51406. . 51488, 51567. . 51733,**  
**51818. . 52033, 52078. . 52294, 52510. . 52743))**  
**/gene="F5114.9"**  
**note="Strong similarity to *Arabidopsis***  
**zeta-crystallin-like protein (gb|249268)."**  
**codon\_start=1**  
**evidence=not\_experimental**  
**/protein\_id="AAB60917.1"**  
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**CPFLVYALLCSPSCFEDRMLYVYMLKELYILVYKQKFLFSLISTSFIFEFVLMQ**  
**RTEFGFLAVRVTOSDDTNWPKPGDIVGIGWEEKMWSLKSDDNQLRNQDDDIPSLH**  
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**QKVELKMGFTAVAGENICCPKRGDSVFSAAAGCAGVOLGOLAKLHGCVYVGASAK**  
**GRIALCKMVSQLSSTESQSQGKRNLYAQRKLEGLQSDHFLHIFPQLEVKRYK**  
**EGKIVVVEDISGGLDAPALVGLFGSKKNIGKQVRYAKE"**  
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**complement|join|53168. . 53386|53596. . 54114, 54461. . 54916))**  
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**note="Strong similarity to *Solanum* polygalacturonase**  
**precursor (gb|U23053)."**  
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**(db\_xref="GI: 2190556"**  
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LOCUS	26	tataaatataacactcacttcatgttagataataatataatcgatcacactata	85				
DEFINITION	ATTAATATAACACTTCATGTAGATAATAATCGATCACACATATA						
ACCESSION	13000						
KEYWORD	86	agtaaaacacttcatttccctcccttcattttataacactataatcgact	145				
REFERENCE	12940	AGTAAAACACTTCATTTCCCTCCTCATTATACACACTATATCGACT	12881				
AUTHORS	QY	146 actataaggcataccatcccgccgtgtactcgatcataaattgttattaaattaaatcc	205				
TITLE	Db	actATAGGCCATCATCCCGTGTACTCGATCATAAATCGTTATTAATAATAC	12821				
JOURNAL	QY	206 tatagtgcaataatctcatagatgtgcataatcaatgttataaaggagacca	265				
NOTE	Db	TATAGATGCTATAATCGATCATCGAGATGATCGATATCAATGTTAAAGGAGACCA	12761				
FEATURES	QY	266 tctaaatgtttttccctccggagccacttcctcgacatgttataaaggagacca	325				
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QUALIFIER	QY	326 cggaaaggcccgatgttagatctcgcaactccggatgttgaggttggccacc	385				
FEATURES	Db	CGGAAAGCGCGAGATGATCTAGCTAGCAACTCGCGAGGTTGGCCACC	12641				
LOCATION	QY	386 ctggtgcatactgtgtggctggcaagctgtcgaaacataataacacacatgtaa	445				
QUALIFIER	Db	CAGGTGTCATACACTGTGTGGCTGGCAAGCTGTCGAACACATAATAACACAGCATGAA	12581				
FEATURES	QY	446 ttctctgtggactgtggatttctatgttataacacacataatcgatgtcc	491				
LOCATION	Db	TTCCTGTCAGTGGCACTGTGGATTTCGTAACACACATCTCATGGCC	1235				
RESULT	AF152096/-8						
LOCUS	AF152096	2483 bp	DNA	linear	PLN 22-DEC-1999		
DEFINITION	Arabidopsis thaliana	flowering locus T (FT) gene, complete cds.					
ACCESSION	AF152096						
KEYWORD	AF152096.1	GI:6117977					
FEATURES	QY	source : thale cress.					
ORGANISM	Arabidopsis thaliana						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.						
AUTHORS	1 (bases 1 to 2483)						
TITLE	Kardailsky, I., Shukla, V.K., Ahn, J.H., Dagenais, N., Christensen, S.K., Nguyen, J.T., Chory, J., Harrison, M.J. and Weigel, D.						
JOURNAL	Activation tagging of the floral inducer FT						
NOTE	Science 286 (5446), 1962-1965 (1999)						
REFERENCE	2 (bases 1 to 2483)						
AUTHORS	Kardailsky, I. and Weigel, D.						
TITLE	Direct Submission						
JOURNAL	Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA						
FEATURES	1. Location/Qualifiers						
LOCATION	source						
QUALIFIER	/organism="Arabidopsis thaliana"						









